

WORLD INTELLECTUAL PROPERTY ORGANIZATION International Bureau



A VINDED THE DATENT COOPERATION TREATY (PC

INTERNATIONAL APPLICATION PUBLIS	HED I	ED UNDER THE PATENT COOPERATION TREATT (PCT			
(51) International Patent Classification 7:		(11) International Publication Number:	WO 00/58473		
C12N 15/12, C07K 14/47, 16/18, G01N 33/566, C12Q 1/68, C12N 15/11, 15/62, A01K 67/027, A61K 38/00	A2	(43) International Publication Date:	5 October 2000 (05.10.00)		
(21) International Application Number: PCT/USC (22) International Filing Date: 31 March 2000 (3		(75) Inventors/Applicants (for U.5 only	est Haven, CT 06516 (US).		

(30) Priority Data: 60/127,607 60/127,636 60/127,728 09/540,763	31 March 1999 (31.03.99) 2 April 1999 (02.04.99) 5 April 1999 (05.04.99) 30 March 2000 (30.03.00)	US US US US
---	--	----------------------

PCT

(63) Related by Continuation (CON) or Continuation-in-Part

(CIP) to Earlier Applications	
ùs	60/127,607 (CIP)
Filed on	31 March 1999 (31.03.99)
US	60/127,636 (CIP)
Filed on	2 April 1999 (02.04.99)
US	60/127,728 (CIP)
Filed on	5 April 1999 (05.04.99)
US	09/540,763 (CIP)
Filed on	30 March 2000 (30.03.00)

(71) Applicant (for all designated States except US): CURAGEN CORPORATION [US/US]; 555 Long Wharf Drive, 11th Floor, New Haven, CT 06511 (US).

01570 (US).

(74) Agent: ELRIFI, Ivor, R.; Mintz, Levin, Cohn, Ferris, Glovsky and Popeo, P.C., One Financial Center, Boston, MA 02111 (US)

(81) Designated States: AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CR, CU, CZ, DE, DK, DM, EE, ES. FL GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, ARIPO patent (GH, GM, KE, LS, MW, SD, SL, SZ, TZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG).

Published

Without international search report and to be republished upon receipt of that report.

(54) Title: NUCLEIC ACIDS INCLUDING OPEN READING FRAMES ENCODING POLYPEPTIDES; "ORFX"

(57) Abstract

The present invention provides open reading frames ORFX, encoding isolated polypeptides, as well as polynucleotides encoding ORFX and antibodies that immunospecifically bind to ORFX or any derivative, variant, mutant, or fragment of the ORFX polypeptides, polynucleotides or antibodies. The invention additionally provides methods in which the ORFX polyneptide, polynucleotide and antibody are used in detection and treatment of a broad range of pathological states, as well as to other uses.

FOR THE PURPOSES OF INFORMATION ONLY

Codes used to identify States party to the PCT on the front pages of pamphlets publishing international applications under the PCT.

٨L	Albania	ES	Spain	LS	Lesotho	SI	Slovenia
AM	Armenia	FI	Finland	LT	Lithuania	SK	Slovakia
AT	Austria	FR	France	LU	Luxembourg	SN	Senegal
ΑU	Australia	GA.	Gabon	LV	Latvia	SZ	Swaziland
ΑZ	Azerbaijan	GB	United Kingdom	MC	Monaco	TD	Chad
BA	Bosnia and Herzegovina	GE	Georgia	MD	Republic of Moldova	TG	Togo
BB	Barbados	GH	Ghana	MG	Madagascar	TJ	Tajikistan
BE	Belgium	GN	Guinca	MK	The former Yugoslav	TM	Turkmenistan
BF	Burkina Paso	GR	Greece		Republic of Macedonia	TR	Turkey
BG	Bulgaria	HU	Hungary	ML	Mali	TT	Trinidad and Tobago
BJ	Benin	IE	Ireland	MN	Mongolia	UA	Ukraine
BR	Brazil	IL	Israel	MR	Mauritania	UG	Uganda
BY	Belarus	IS	Iceland	MW	Malawi	US	United States of America
CA	Canada	IT	Italy	MX	Mexico	UZ	Uzbekistan
CF	Central African Republic	JP	Japan	NE	Niger	VN	Vict Nam
CG	Congo	KE	Kenya	NL	Netherlands	YU	Yugoslavia
CH	Switzerland	KG	Kyrgyzstan	NO	Norway	zw	Zimbabwe
CI	Côte d'Ivoire	KP	Democratic People's	NZ	New Zealand	2	Euronome
CM	Cameroon		Republic of Korea	PL	Poland		
CN	China	KR	Republic of Korea	PT	Portugal		
CU	Cuba	KZ	Kazakstan	RO	Romania		
cz	Czech Republic	LC	Saint Lucia	RU	Russian Federation		
DB	Germany	и	Liechtenstein	SD	Sudan		
DK	Denmark	LK	Sri Lanka	SE	Sweden		
EE	Estonia	LR	Liberia	SG	Singapore		

What is claimed is:

 An isolated nucleic acid molecule encoding a polypeptide comprising an amina acid sequence that is at least 85% identical to a polypeptide including an amino acid sequence selected from the group consisting of SEQ ID NO:2n, wherein n is any integer 1-3161, or the complement thereof.

- 2. The isolated nucleic acid molecule of claim 1, said molecule hybridizing under stringent conditions to a nucleic acid sequence complementary to a nucleic acid molecule comprising the sequence of nucleotides selected from the group consisting of SEQ ID NO:2n-wherein n is any integer 1-3161, or the complement thereof.
- 3. The isolated nucleic acid molecule of claim 1, said molecule encoding a polypeptide comprising the amino acid sequence selected from the group consisting of SEQ II NO: 2n, wherein n is any integer 1-3161, or an amino acid sequence comprising one or more conservative substitutions in the amino acid sequence selected from the group consisting of SI ID NO: 2n
- 4. The isolated nucleic acid molecule of claim 1, wherein said molecule encodes: polypeptide comprising the amino acid sequence selected from the group consisting of SEQ II NO: 2n, wherein n is any integer 1-3161.
- 5. The isolated nucleic acid molecule of claim 1, wherein said molecule comprise the sequence of nucleotides selected from the group consisting of SEQ ID NO:2n-1, wherein sany integer 1-3161, or the complement thereof.
- 6. An oligonucleotide less than 100 nucleotides in length and comprising at least contiguous nucleotides selected from the group consisting of SEQ ID NO:2n-1, wherein n is a integer 1-3161, or the complement thereof.
 - A vector comprising the nucleic acid molecule of claim 1.

- 8. The vector of claim 7, wherein said vector is an expression vector.
- 9 A host cell comprising the isolated nucleic acid molecule of claim 1.
- 10. A substantially purified polypeptide comprising an amino acid sequence at least 80% identical to a polypeptide comprising the amino acid sequence selected from the group consisting of SEO ID NO: 2n. wherein n is any integer 1-3161.
- 11. The polypeptide of claim 10, wherein said polypeptide comprises the amino acid sequence selected from the group consisting of SEQ ID NO: 2n, wherein n is any integer 1-3161.
 - 12. An antibody that selectively binds to the polypeptide of claim 10.
- 13. A pharmaceutical composition comprising a therapeutically or prophylactically effective amount of a therapeutic selected from the group consisting of:
 - a) the nucleic acid of claim 1;
 - b) the polypeptide of claim 10; and
 - the antibody of claim 12:
 - and a pharmaceutically acceptable carrier.
- A kit comprising in one or more containers, a therapeutically or prophylactically
 effective amount of the pharmaceutical composition of claim 13.
- 15. A method of producing the polypeptide of claim 10, said method comprising culturing the host cell of claim 9 under conditions in which the nucleic acid molecule is expressed.
- 16. A method of detecting the presence of the polypeptide of claim 10 in a sample, comprising contacting the sample with a compound that selectively binds to said polypeptide under conditions allowing the formation of a complex between said polypeptide and said

compound, and detecting said complex, if present, thereby identifying said polypeptide in said sample.

- 17. A method of detecting the presence of a nucleic acid molecule of claim 1 in a sample, the method comprising contacting the sample with a nucleic acid probe or primer that selectively binds to the nucleic acid molecule and determining whether the nucleic acid probe or primer bound to the nucleic acid molecule of claim 1 is present in the sample.
- 18. A method for modulating the activity of the polypeptide of claim 10, the method comprising contacting a cell sample comprising the polypeptide of claim 10 with a compound that binds to said polypeptide in an amount sufficient to modulate the activity of the polypeptid
- 19. The use of a therapeutic in the manufacture of a medicament for treating a syndrome associated with a ORFX-associated disorder, wherein said therapeutic is selected fro the group consisting of:
 - a) the nucleic acid of claim 1;
 - b) the polypeptide of claim 10; and
 - the antibody of claim 12.
- 20. A method for screening for a modulator of activity or of latency or predispositio to an ORFX-associated disorder, said method comprising:
 - a) contacting a test compound with the polypeptide of claim 10; and
- b) determining if said test compound binds to said polypeptide,
 wherein binding of said test compound to said polypeptide indicates the test compound is a modulator of activity or of latency or predisposition to an ORFX-associated disorder.
- A method for screening for a modulator of activity or of latency or predisposition
 to an ORFX-associated disorder, said method comprising:
 - administering a test compound to a test subject at an increased risk ORFXassociated disorder, wherein said test subject recombinantly expresses a polypeptide encoded by the nucleotide of claim 1;

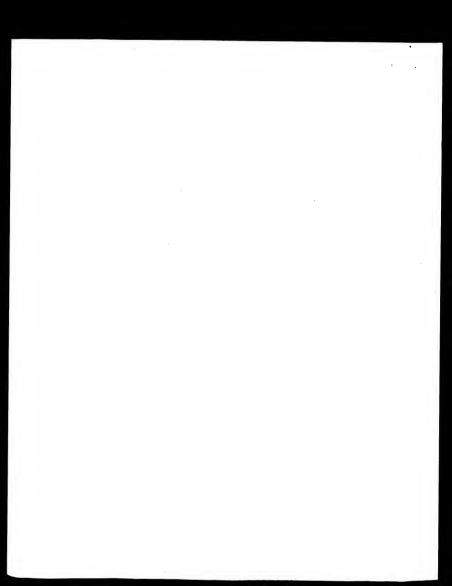
- measuring expression the activity of said protein in said test subject;
- measuring the activity of said protein in a control subject that recombinantly expresses said protein and is not at increased risk for an ORFX-associated disorder; and
- d) comparing expression of said protein in said test subject and said control subject, wherein a change in the activity of said protein in said test subject relative to said control subject indicates the test compound is a modulator or of latency of predisposition to an ORFX-associated disorder.
- 22. The method of claim 20, wherein said test animal is a recombinant test animal that expresses a test protein transgene or expresses said transgene under the control of a promoter at an increased level relative to a wild-type test animal, and wherein said promoter is not the native gene promoter of said transgene.
- 23. A method for determining the presence of or predisposition to a disease associated with altered levels of a polypeptide of claim 11 in a subject, the method comprising:
 - a) measuring the amount of the polypeptide in a sample from said subject; and
 - comparing the amount of said polypeptide in step (a) to the amount of the polypeptide present in a control sample,

wherein an alteration in the level of the polypeptide in step (a) as compared to the control sample indicates the presence of or predisposition to a disease in said subject.

- 24. The method of claim 23, wherein said subject is a human.
- 25. A method for determining the presence of or predisposition to a disease associated with altered levels the nucleic acid molecule of claim 1 in a subject, the method comprising:
 - measuring the amount of the nucleic acid in a sample from the mammalian subject; and
 - comparing the amount of said nucleic acid in step (a) to the amount of the nucleic acid present in a control sample,

wherein an alteration in the level of the nucleic acid in step (a) as compared to the corsample indicates the presence of or predisposition to said disease in said subject.

- 26. The method of claim 25, wherein said subject is a human.
- 27. A method of treating or preventing a pathological condition associated with an ORFX-associated disorder in a subject, the method comprising administering to said subject polypeptide of claim 10 in an amount sufficient to alleviate or prevent said pathological condition.
 - 28. The method of claim 27, wherein said subject is a human.
- 29. A method of treating or preventing a pathological condition associated with ar ORFX-associated disorder in a subject, the method comprising administering to said subject nucleic acid molecule of claim 1 in an amount sufficient to alleviate or prevent said pathological condition.
 - 30. The method of claim 29, wherein said subject is a human.
- 31. A method of treating or preventing a pathological condition associated with ar ORFX-associated disorder in a subject, the method comprising administering to said subject t antibody of claim 12 in an amount sufficient to alleviate or prevent said pathological condition.
 - 32. The method of claim 31, wherein said subject is a human.



<213> Homo sapiens

<210> 361 <211> 453

<212> DNA

<213> Homo sapiens

<400> 361
gctttgcagg aggaaatct tatcttggc tgcaagatga ggctgagcta cctgagcagc
60
cggacccctg gctacaaatc tgtcctgagg atcagctca cccaccgac catcccttc
120
aacctcatga aggtgaccct catgatagc gtggagggc gcctctcag gaagtggtt
180
gctgcagccc cagacctgtc ctattatttc atttgggaca agacagacgt ctacaaccag
240
aaggtgtttg ggctttcaga agccttgtt tccgtgggtt atgaatatga atcctgcca
300
gatctcaatcc tgtgggaaaa aagaacaac gtgctgcagg gctatgaaat tgacgctc
360
aaggttggag gatggagcct agacaacat catgccctca acattcaaag tggcatcctg
420
cacaaaaqga atqqqaaa cagtttgtg tct

<210> 362

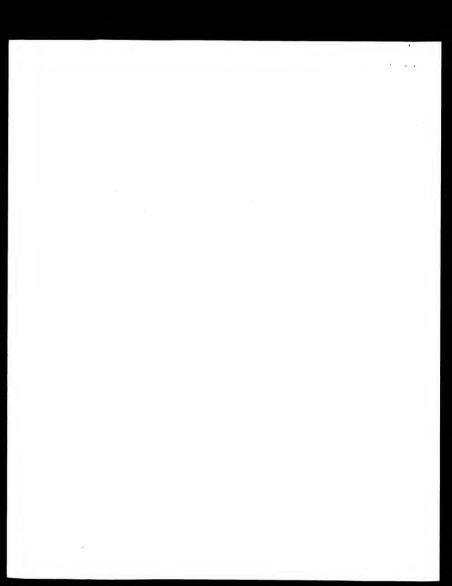
453

<211> 151 <212> PRT

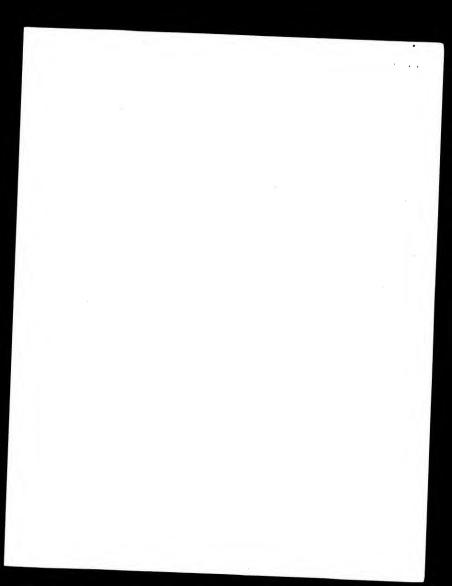
<213> Homo sapiens

<400> 362

<4000 J62</p>
Ala Leu Gln Glu Glu Ile Ser Ile Ser Gly Cys Lys Met Arg Leu Ser 1
1 5
Tyr Leu Ser Ser Arg Thr Pro Gly Tyr Lys Ser Val Leu Arg Ile Ser 20
25
30
Leu Thr His Pro Thr Ile Pro Phe Asn Leu Met Lys Val His Leu Met 15
40
Val Ala Val Glu Gly Arg Leu Phe Arg Lys Trp Phe Ala Ala Ala Pro 50
Asp Leu Ser Tyr Tyr Phe Ile Trp Asp Lys Thr Asp Val Tyr Asn Gln



```
Lys Val Phe Gly Leu Ser Glu Ala Phe Val Ser Val Gly Tyr Glu Tyr
Glu Ser Cys Pro Asp Leu Ile Leu Trp Glu Lys Arg Thr Thr Val Leu
Gln Gly Tyr Glu Ile Asp Ala Ser Lys Leu Gly Gly Trp Ser Leu Asp
                            120
Lys His His Ala Leu Asn Ile Gln Ser Gly Ile Leu His Lys Gly Asn
                        135
Gly Glu Asn Gln Phe Val Ser
                    150
145
<210> 363
<211> 502
 <212> DNA
<213> Homo sapiens
ggtaccaaaa aagtttgcca cagtattcac actccaggtc tccataaacc ttccagatcc
gotcacacaa gotggtgtto atttgcttct totgtaaact gttcaggaco ttcatgaaag
 eggtgatgee tgaceggtge teaggggeag etttgeaaga gteaggetga tgtgtgatgg
 tgtccccacc accagctact ggagggagga ggtctgaggc ctcagctggg tttgacctga
 gacacctget gggatetggg teaccagetg aaageacage catgttetge eetteeecta
 gggggetetg ggegecatgg ettteetgat etgacecage actetgggee ttggacagea
 gtagtgtgat cacttcacct tgcgtctgga ctgagcttct gtgctgcatg tctgggggct
 teteaggage ageatgagee tetgeggagg aggtateatt ttteaacaaa aaateatetg
 aaaccacctc ttgagaatgc ag
 502
 <210> 364
 <211> 136
  <212> PRT
 <213> Homo sapiens
 Met Gln His Arg Ser Ser Val Gln Thr Gln Gly Glu Val Ile Thr Leu
  Leu Leu Ser Lys Ala Gln Ser Ala Gly Ser Asp Gln Glu Ser His Gly
  Ala Gln Ser Pro Leu Gly Glu Gly Gln Asn Met Ala Val Leu Ser Ala
  Gly Asp Pro Asp Pro Ser Arg Cys Leu Arg Ser Asn Pro Ala Glu Ala
  Ser Asp Leu Leu Pro Pro Val Ala Gly Gly Asp Thr Ile Thr His
                      70
  Gln Pro Asp Ser Cys Lys Ala Ala Pro Glu His Arg Ser Gly Ile Thr
```



```
TD
     HSM010618 standard; RNA; EST; 718 BP.
xx
ÁC
     AL045768:
                    XP-002237532
ХX
                                                                P.D. 20 - 02 - 200
sv
     AT-045768 1
xx
     12-MAR-1999 (Rel. 59, Created)
DТ
DT
     20-FEB-2000 (Rel. 62, Last updated, Version 4)
XX
DE
     Homo sapiens mRNA; EST DKFZp434F206_r1 (from clone DKFZp434F206)
ХX
KW
     EST: expressed sequence tag.
ХX
os
     Homo sapiens (human)
oc
     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
oc
     Eutheria; Primates; Catarrhini; Hominidae; Homo.
ХX
RN
RP
     1-718
RA
     Koehrer K., Beyer A., Mewes H.W., Gassenhuber J., Wiemann S.;
PΨ
RT.
     Submitted (18-FEB-2000) to the EMBL/GenBank/DDBJ databases.
RI.
     MIPS, Am Klopferspitz 18a, D-82152 Martinsried, GERMANY
xx
DR
     RZPD; DKFZp434F206: DKFZp434F206.
DR
     UNILIB; 1752; 1752.
ХX
CC
     This is the 5' sequence of the clone insert
CC
     Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
CC
     Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
CC
     sequenced by BMFZ (Biomedical Research Center at the Charite,
CC
     Berlin/Germany) within the cDNA sequencing consortium of the
CC
     German Genome Project.
CC
     s1 sequence also available.
CC
     This clone (DKFZp434F206) is available at the RZPD in Berlin.
CC
     Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6,
CC
     14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
хx
FH
     Key
                     Location/Oualifiers
FH
FT
     source
                     1.,718
FT
                     /db xref="taxon:9606"
FT
                     /db_xref="RZPD:DKFZp434F206"
FT
                     /db_xref="UNILIB:1752"
FT
                     /organism="Homo sapiens"
FT
                     /clone="DKFZp434F206"
FT
                     /clone_lib="434 (synonym: htes3). Vector pSport1: host
FT
                     DH10B; sites NotI + SalI"
FT
                     /dev stage="adult"
FT
                     /tissue type="testis"
XX
     Sequence 718 BP; 183 A; 196 C; 198 G; 141 T; 0 other:
     getteatgae agatgttaae agetggetge teacetttgg attecageta cacaacgtga
                                                                               60
     tccctggtta tcccaaacca gacatggatg ccatggaacc ctcctacgag cttatccaca
                                                                              120
     cacagatgaa aacgcaggag tgggacaaca gcaagtctat cctcggggta cagtgtgaag
                                                                              180
     tacagaagca gctcaaggcc tttgtcacct tagaacggtt tgaccagctc tatggctcca
                                                                              240
     caatcaccag ctgccagcag gctccaaaga ccaagaagtt tgcatccagc ggctcagtct
                                                                              300
     ttggcaaggg ggtcaagttt gccttgaagg atggccgagt gaccacagac atcatcagtg
                                                                              360
     tggccaatga ggatgggcga agggttgctg ccatcttgaa ccatgcccac tacctagaga
                                                                              420
     acctgcactt caccattgat ggggtggata cccattactt tgtgaaacca ggaccttcag
                                                                              480
     aaggtgacct ggccatcctg ggcctcagtg gggggcggcg aaccctggag aatggggtca
                                                                              540
     acgtcactgt gtcccagatc aacacagtac ttaatggcag gactagacgc tacacagaca
```

tccagctcca gtacggggca ctgtgcttga acacacgcta cgggacaacg ttggatgagg

agaaggcacg ggtcctggag ctgtcccggc agagagccgt gcgccaagcg tgggcccc

600

660

718

